

## SEQUENCE LISTING

<110> Diversa Corporation  
 Hitchman, Timothy  
 Robertson, Dan  
 Gray, Kevin  
 Hiraiwa, Masao  
 Phillips, Yoko

<120> LACCASES, NUCLEIC ACIDS ENCODING THEM AND METHODS FOR MAKING AND USING THEM

<130> 564462012640

<140> To Be Assigned

<141> Concurrently Herewith

<150> 60/494,472

<151> 2003-08-11

<160> 26

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 1542

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 1

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cgcgatctcc	ctccaaccgc	cttgtggggc	tataacgggt	tattccccgc	tcccaccatt	180
aaggccaaaa	gaaatgaaaa	cgtttatgtg	aaatggatga	ataaccttcc	ttcagagcat	240
tttcttcgga	ttgatcacac	cattcatcac	agtgcagcc	agcatgccga	acccgaggtg	300
aaaaccgtcg	ttcatttaca	cggcggcgtc	actccagatg	acagcgacgg	ttatcctgag	360
gcctggtttt	ctaaagactt	tgaacaaaca	ggcccttatt	ttaaacgaga	ggtttaccat	420
tatccaaatc	agcagcgcg	agctatttta	tggtatcacg	atcatgctat	ggcgctcacg	480
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aatgaagatg	gctctttatt	ttatccgagc	ggaccggaaa	acccttcacc	gtcactgcct	660
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1542

&lt;210&gt; 2

&lt;211&gt; 514

&lt;212&gt; PRT

&lt;213&gt; Unknown

&lt;220&gt;

&lt;223&gt; Obtained from an environmental sample

&lt;400&gt; 2

Met	Thr	Arg	Glu	Lys	Phe	Val	Asp	Ala	Leu	Pro	Ile	Pro	Asp	Thr	Leu
1				5					10					15	
Lys	Pro	Val	Gln	Gln	Ser	Lys	Asp	Ser	Thr	Tyr	Tyr	Glu	Val	Thr	Met
			20					25					30		
Glu	Glu	Cys	Tyr	His	Gln	Leu	His	Arg	Asp	Leu	Pro	Pro	Thr	Arg	Leu
		35					40					45			
Trp	Gly	Tyr	Asn	Gly	Leu	Phe	Pro	Gly	Pro	Thr	Ile	Lys	Ala	Lys	Arg
	50					55					60				
Asn	Glu	Asn	Val	Tyr	Val	Lys	Trp	Met	Asn	Asn	Leu	Pro	Ser	Glu	His
65					70					75					80
Phe	Leu	Pro	Ile	Asp	His	Thr	Ile	His	His	Ser	Asp	Ser	Gln	His	Ala
				85						90				95	
Glu	Pro	Glu	Val	Lys	Thr	Val	Val	His	Leu	His	Gly	Gly	Val	Thr	Pro
			100					105					110		
Asp	Asp	Ser	Asp	Gly	Tyr	Pro	Glu	Ala	Trp	Phe	Ser	Lys	Asp	Phe	Glu
		115					120					125			
Gln	Thr	Gly	Pro	Tyr	Phe	Lys	Arg	Glu	Val	Tyr	His	Tyr	Pro	Asn	Gln
	130					135					140				
Gln	Arg	Gly	Ala	Ile	Leu	Trp	Tyr	His	Asp	His	Ala	Met	Ala	Leu	Thr
145					150					155					160
Arg	Leu	Asn	Val	Tyr	Ala	Gly	Leu	Ile	Gly	Ala	Tyr	Ile	Ile	His	Glu
				165					170					175	
Pro	Lys	Glu	Lys	Arg	Leu	Lys	Leu	Pro	Ser	Gly	Glu	Tyr	Asp	Val	Pro
			180					185					190		
Leu	Leu	Ile	Thr	Asp	Arg	Thr	Ile	Asn	Glu	Asp	Gly	Ser	Leu	Phe	Tyr
		195					200					205			
Pro	Ser	Gly	Pro	Glu	Asn	Pro	Ser	Pro	Ser	Leu	Pro	Asn	Pro	Ser	Ile
		210				215					220				
Val	Pro	Ala	Phe	Cys	Gly	Asp	Thr	Ile	Leu	Val	Asn	Gly	Lys	Ala	Trp
225					230					235					240
Pro	Tyr	Met	Glu	Val	Glu	Pro	Arg	Lys	Tyr	Arg	Phe	Arg	Val	Ile	Asn
				245					250					255	
Ala	Ser	Asn	Thr	Arg	Thr	Tyr	Asn	Leu	Ser	Leu	Asp	Asn	Gly	Gly	Glu
			260					265					270		
Phe	Ile	Gln	Ile	Gly	Ser	Asp	Gly	Gly	Leu	Leu	Pro	Arg	Ser	Val	Lys
		275					280					285			
Leu	Asn	Ser	Phe	Ser	Ile	Ala	Pro	Ala	Glu	Arg	Phe	Asp	Ile	Leu	Ile
		290				295					300				
Asp	Phe	Ala	Ala	Phe	Glu	Gly	Gln	Ser	Ile	Ile	Leu	Ala	Asn	Ser	Glu
305					310					315					320
Gly	Cys	Gly	Gly	Asp	Val	Asn	Pro	Glu	Thr	Asp	Ala	Asn	Ile	Met	Gln
				325					330					335	
Phe	Arg	Val	Thr	Lys	Pro	Leu	Ala	Gln	Lys	Asp	Glu	Ser	Arg	Lys	Pro
			340					345					350		
Lys	Tyr	Leu	Ala	Ser	Tyr	Pro	Ser	Val	Arg	His	Glu	Arg	Ile	Gln	Asn
		355					360					365			
Leu	Arg	Thr	Leu	Lys	Leu	Ala	Gly	Thr	Gln	Asp	Gln	Tyr	Gly	Arg	Pro
		370				375					380				

Val Leu Leu Leu Asn Asn Lys Arg Trp His Asp Pro Val Thr Glu Ala  
 385 390 395 400  
 Pro Lys Ala Gly Ser Thr Glu Ile Trp Ser Ile Ile Asn Pro Thr Arg  
 405 410 415  
 Gly Thr His Pro Ile His Leu His Leu Val Ser Phe Arg Val Leu Asp  
 420 425 430  
 Arg Arg Pro Phe Asp Thr Ala Arg Phe Glu Glu Arg Gly Glu Leu Ala  
 435 440 445  
 Tyr Thr Gly Pro Ala Val Pro Pro Pro Pro Ser Glu Lys Gly Trp Lys  
 450 455 460  
 Asp Thr Val Gln Ser His Ala Gly Glu Val Leu Arg Ile Ala Val Thr  
 465 470 475 480  
 Phe Gly Pro Tyr Thr Gly Arg Tyr Val Trp His Cys His Ile Leu Glu  
 485 490 495  
 His Glu Asp Tyr Asp Met Met Arg Pro Met Asp Val Ile Asp Pro His  
 500 505 510  
 Lys Ser

&lt;210&gt; 3

&lt;211&gt; 1626

&lt;212&gt; DNA

&lt;213&gt; Unknown

&lt;220&gt;

&lt;223&gt; Obtained from an environmental sample

&lt;400&gt; 3

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cttgctcgcg ctggtgcgtc cggctctctg acgctgcgcg aggtccgggc gcaaccccgt      120
gctgcgaatc cgcagttcat cccggacctc gagatccagt tgaacgctcg ggaagatcat      180
gtgtcgatcc tgcctggacc actcactcgc gtctggcggt acgacggcaa agtcgtgaag      240
ggcgatccgg gcaacctggc tttcctgtcg aacggttatt taccggtggg gcgcgtgcgg      300
cgcgacacaga aagtgcgcat cgatttcgtc aaccagttag ctgagccgac catcatccac      360
tgccatggcc tgtacgtgcc agcagcaatg gatggacatc cgcgcaatgc gggttcgacc      420
ggcgagcact acgtgtacga gttcgagatc gcccaaccagg cagggacgta ctggtttcat      480
gcgcaccccc acggtcgtac gggagcacia atttacttcg gactggcggg ggtattgatc      540
gtcgacgatg aggaggcggc cgccgggttg cccgaaggtc cgtacgatgt accgctcgtg      600
attcaggacc gcacgttcga cgatcggaac cagttcacgt atctcgccga aggcaatgag      660
gggatgatgg gcggcatgat gggcaacggc ggcatgatgg gacgcggggg catgatggc      720
ggaggcgcca tggggcagat gatggcgcg atgatgggtt tcctcggcga ccggattctc      780
gtcaacggca agcccgactt cgtgctgccg gtggctgccc gtgcctatcg ccttcgtttg      840
ctgaatgggt cgaacacgcg tatctacaag ctgctgga gcgaccggac acccctcacg      900
gtaatcggtc cggacggcgg actgctggaa cggccggtga cgcgccaata cgtcacgctg      960
gcgcggcgcc agcgcgtgga cgtctgggtg gatttcagtc gatggccggt cggcacgaag     1020
ctgacgctgc agagtctggc gttcgacggc gtcctggcca tgggcggcat gatcggcaac     1080
acctcgttac cgagcggcgc gtcgttcccg gtcctgaagg tcggcgctcg ccagcgtgcg     1140
aacacaaaga tggaaactgcc ggcgcggtc gcacgcgtgc caccggtgcg ccctcaggac     1200
gccgtcaatg cgcacaatcc gaaggtgttc aacatcacga tgggcatgat ggtctggggc     1260
gtcaacgggc gtcgcttcga aatgaacggg gtggcgaaaa cggagaccgt gagacgcaac     1320
agcacggaaa tctgggagtt ccgcaacgag gaatcgatga tgctgatggc ccattcgatg     1380
cacgttcacg ggctgcagtt ccgtgtgctg gagcgtaccg tccagccgga ttccagagcc     1440
ggttaccgca cgctggcagc gggactgggt gatgatggct ggaaagacac cgtgctattg     1500
atgcccgggt agcgtatccg cctgctgctc cggttcgcga gctacacggg cctgtttctt     1560
taccattgtc acatgctgga gcacgaagat tccggattga tgcgtaacta cctgatccag     1620
acgtaa
  
```

&lt;210&gt; 4

&lt;211&gt; 541

&lt;212&gt; PRT

&lt;213&gt; Unknown

&lt;220&gt;

&lt;223&gt; Obtained from an environmental sample

&lt;221&gt; SIGNAL

&lt;222&gt; (1)...(37)

&lt;400&gt; 4

```

Met Leu Arg Pro Glu Asp Ala Thr Arg Arg Ala Phe Leu His Ala Ala
 1          5          10          15
Thr Met Ser Cys Leu Val Ala Ala Gly Ala Ser Gly Leu Leu Thr Leu
          20          25          30
Arg Glu Val Arg Ala Gln Pro Arg Ala Ala Asn Pro Gln Phe Ile Pro
          35          40          45
Asp Leu Glu Ile Gln Leu Asn Ala Arg Glu Asp His Val Ser Ile Leu
          50          55          60
Pro Gly Pro Leu Thr Arg Val Trp Arg Tyr Asp Gly Lys Val Val Lys
          65          70          75          80
Gly Asp Pro Gly Asn Leu Ala Phe Leu Ser Asn Gly Tyr Leu Pro Val
          85          90          95
Val Arg Val Arg Arg Gly Gln Lys Val Arg Ile Asp Phe Val Asn Gln
          100          105          110
Leu Ala Glu Pro Thr Ile Ile His Trp His Gly Leu Tyr Val Pro Ala
          115          120          125
Ala Met Asp Gly His Pro Arg Asn Ala Val Ser Thr Gly Glu His Tyr
          130          135          140
Val Tyr Glu Phe Glu Ile Ala Asn Gln Ala Gly Thr Tyr Trp Phe His
          145          150          155          160
Ala His Pro Asp Gly Arg Thr Gly Ala Gln Ile Tyr Phe Gly Leu Ala
          165          170          175
Gly Val Leu Ile Val Asp Asp Glu Glu Ala Ala Ala Gly Leu Pro Glu
          180          185          190
Gly Pro Tyr Asp Val Pro Leu Val Ile Gln Asp Arg Thr Phe Asp Asp
          195          200          205
Arg Asn Gln Phe Thr Tyr Leu Ala Glu Gly Asn Glu Gly Met Met Gly
          210          215          220
Gly Met Met Gly Asn Gly Gly Met Met Gly Arg Gly Gly Met Met Gly
          225          230          235          240
Gly Gly Gly Met Gly Gln Met Met Ala Arg Met Met Gly Phe Leu Gly
          245          250          255
Asp Arg Ile Leu Val Asn Gly Lys Pro Asp Phe Val Leu Pro Val Ala
          260          265          270
Ala Arg Ala Tyr Arg Leu Arg Leu Leu Asn Gly Ser Asn Thr Arg Ile
          275          280          285
Tyr Lys Leu Ala Trp Ser Asp Arg Thr Pro Leu Thr Val Ile Gly Thr
          290          295          300
Asp Gly Gly Leu Leu Glu Arg Pro Val Thr Arg Gln Tyr Val Thr Leu
          305          310          315          320
Ala Pro Ala Glu Arg Val Asp Val Trp Val Asp Phe Ser Arg Trp Pro
          325          330          335
Val Gly Thr Lys Leu Thr Leu Gln Ser Leu Ala Phe Asp Gly Val Leu
          340          345          350
Ala Met Gly Gly Met Ile Gly Asn Thr Ser Leu Pro Ser Gly Ala Ser
          355          360          365
Phe Pro Val Leu Lys Val Gly Val Asp Gln Arg Ala Asn Thr Lys Met
          370          375          380
Glu Leu Pro Ala Arg Leu Ala Ser Leu Pro Pro Val Arg Pro Gln Asp

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385		390		395		400
Ala Val Asn Ala His	Asn Pro Lys Val Phe Asn Ile Thr Met Gly Met					
	405		410		415	
Met Val Trp Gly Val	Asn Gly Arg Arg Phe Glu Met Asn Gly Val Ala					
	420		425		430	
Lys Thr Glu Thr Val	Arg Arg Asn Ser Thr Glu Ile Trp Glu Phe Arg					
	435		440		445	
Asn Glu Glu Ser Met Met	Leu Met Ala His Ser Met His Val His Gly					
	450		455		460	
Leu Gln Phe Arg Val	Leu Glu Arg Thr Val Gln Pro Asp Phe Arg Ala					
	465		470		475	
Gly Tyr Arg Thr Leu	Ala Ala Gly Leu Val Asp Asp Gly Trp Lys Asp					
	485		490		495	
Thr Val Leu Leu Met	Pro Gly Glu Arg Ile Arg Leu Leu Leu Arg Phe					
	500		505		510	
Ala Ser Tyr Thr Gly	Leu Phe Leu Tyr His Cys His Met Leu Glu His					
	515		520		525	
Glu Asp Ser Gly Leu	Met Arg Asn Tyr Leu Ile Gln Thr					
	530		535		540	

&lt;210&gt; 5

&lt;211&gt; 1584

&lt;212&gt; DNA

&lt;213&gt; Bacteria

&lt;400&gt; 5

atggacaggc	gtaaaatttat	aaaaacttct	ctcttttccg	cccttggcctt	ttcggttggg	60
ggactttccc	tccttttctg	cggagggggg	ggtacaaccg	gaagttcctc	gggtcagggc	120
agcggaaatt	tgagtaaaca	atccctcaat	atccccgat	acttcctttt	tcccgatgga	180
cagcgagtaa	gtataaccgc	aaagtggaca	acccttgagg	taatccccgg	aaagtcgacg	240
gatatgctcg	tttacgagat	tgataatgag	tacaaccccc	tcataatttct	cagaaagggg	300
caaactttca	gtgctgactt	tgtgaataac	tccggagaag	actcaataat	acactggcac	360
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ggaggactgc	tggacactcc	gaaggagggt	aatgaaatct	tagtagctcc	gggagagaga	900
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tttgaagtta	tggagttcag	ggttacaaag	gattctgctt	acgacaaaag	tattcctcaa	1140
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ggcatgagga	gaatgggttt	cacgattaac	ggagaaacgt	gggaagacgg	ctacgcaaat	1260
ccgcaggaca	taaacaatcc	gaagggttct	tttgaacaga	acaacggcga	cgtggtgatt	1320
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caagttctag	aaaggagctt	gggacctttg	agggtctacg	acctcggctg	gaaggatacg	1440
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gagcaccaga	tataccttct	tcactgccac	attctcgaac	accacgacga	ggggatgatg	1560
gtcaattaca	gggtaaacgc	ctga				1584

&lt;210&gt; 6

&lt;211&gt; 527

&lt;212&gt; PRT

&lt;213&gt; Bacteria

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; (1)...(37)

&lt;221&gt; DOMAIN

&lt;222&gt; (56)...(185)

&lt;223&gt; Multicopper oxidase

&lt;400&gt; 6

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Met Asp Arg Arg Lys Phe Ile Lys Thr Ser Leu Phe Ser Ala Leu Gly
 1      5      10      15
Phe Ser Val Gly Leu Ser Leu Leu Ser Cys Gly Gly Gly Gly Thr
      20      25      30
Thr Gly Ser Ser Ser Gly Gln Gly Ser Gly Thr Leu Ser Lys Gln Ser
      35      40      45
Leu Asn Ile Pro Gly Tyr Phe Leu Phe Pro Asp Gly Gln Arg Val Ser
      50      55      60
Ile Thr Ala Lys Trp Thr Thr Leu Glu Val Ile Pro Gly Lys Ser Thr
      65      70      75      80
Asp Met Leu Val Tyr Glu Ile Asp Asn Glu Tyr Asn Pro Val Ile Phe
      85      90      95
Leu Arg Lys Gly Gln Thr Phe Ser Ala Asp Phe Val Asn Asn Ser Gly
      100      105      110
Glu Asp Ser Ile Ile His Trp His Gly Phe Arg Ala Pro Trp Lys Ser
      115      120      125
Asp Gly His Pro Tyr Tyr Ala Val Lys Asp Gly Glu Thr Tyr Ser Tyr
      130      135      140
Pro Asp Phe Thr Ile Ile Asp Arg Ser Gly Thr Tyr Phe Tyr His Pro
      145      150      155      160
His Pro His Gly Arg Thr Gly Tyr Gln Val Tyr Tyr Gly Leu Ala Gly
      165      170      175
Met Ile Ile Ile Glu Asp Glu Asp Glu Asp Asn Leu Lys Gln Ala Leu
      180      185      190
Asp Leu Glu Tyr Gly Val Ile Asp Ile Pro Leu Ile Ile Gln Asp Lys
      195      200      205
Thr Phe Asp Ser Ser Gly Gln Leu Val Tyr Asn Pro Met Gly His Met
      210      215      220
Gly Phe Trp Gly Asp Thr Ile Leu Val Asn Leu Thr Pro Asn Pro Tyr
      225      230      235      240
Met Asp Val Glu Arg Lys Ile Tyr Arg Phe Arg Ile Leu Asn Gly Ser
      245      250      255
Asn Ala Arg Pro Tyr Arg Leu Ala Leu Leu Arg Gly Asn Gln Arg Met
      260      265      270
Arg Phe Trp Val Ile Gly Val Glu Gly Gly Leu Leu Asp Thr Pro Lys
      275      280      285
Glu Val Asn Glu Ile Leu Val Ala Pro Gly Glu Arg Ile Asp Ile Leu
      290      295      300
Val Asp Phe Arg Asp Ala Ser Val Asn Asp Val Ile Lys Leu Tyr Asn
      305      310      315      320
Phe Pro His Asn Leu Ile Gly Met Gly Met Ile Gly Met Arg Met Gly
      325      330      335
Met Gly Met Glu Arg Gly Met Gly Met Gly Asn Gly Met Asn Met Asp
      340      345      350
Met Gly Met Ala Asp Asn Ser Glu Phe Glu Val Met Glu Phe Arg Val
      355      360      365
Thr Lys Asp Ser Ala Tyr Asp Lys Ser Ile Pro Gln Arg Leu Ser Glu
      370      375      380
Val Thr Pro Ile Asn Thr Asp Gly Ala Gln Val Gln Arg Ile Thr Leu
      385      390      395      400

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<210> 8
<211> 491
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample
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&lt;221&gt; SIGNAL

&lt;222&gt; (1)...(31)

&lt;221&gt; DOMAIN

&lt;222&gt; (190)...(336)

&lt;223&gt; Multicopper oxidase

&lt;400&gt; 8

Met	Asp	Gly	Phe	Val	Glu	Ser	Arg	Arg	Glu	Phe	Leu	Arg	Thr	Thr	Gly	1	5	10	15
Met	Thr	Ala	Gly	Ala	Met	Leu	Phe	Ser	Ser	Gln	Asn	Leu	Phe	Ala	Ala	20	25	30	
Ala	Ala	Glu	Ala	Ala	Ala	Asp	Tyr	Thr	Val	Arg	Ile	Lys	Ala	Ala	Pro	35	40	45	
Ile	Glu	Ile	Ala	Ser	Asp	Lys	Ile	Leu	Ser	Thr	Ile	Thr	Tyr	Asn	Gly	50	55	60	
Gln	Phe	Pro	Gly	Pro	Leu	Ile	Arg	Leu	Lys	Glu	Gly	Arg	Gln	Val	Thr	65	70	75	80
Val	Asp	Ile	Phe	Asn	Glu	Thr	Asp	Thr	Pro	Glu	Gln	Leu	His	Trp	His	85	90	95	
Gly	Gln	Phe	Val	Ser	Pro	Asp	Val	Asp	Gly	Ala	Ala	Glu	Glu	Gly	Thr	100	105	110	
Pro	Tyr	Ile	Pro	Ala	His	Gly	Gln	Arg	Arg	Ile	Met	Phe	Thr	Pro	Gly	115	120	125	
Pro	Ala	Gly	Leu	Arg	Phe	Tyr	His	Thr	His	Asn	Arg	Ala	Gly	Ala	Asp	130	135	140	
Leu	Ser	Leu	Gly	Gln	Tyr	Ser	Gly	Gln	Val	Gly	Pro	Val	Tyr	Ile	Glu	145	150	155	160
Pro	Lys	Glu	Asn	Pro	Gly	Arg	Tyr	Asp	Arg	Glu	Val	Phe	Leu	Val	Leu	165	170	175	
Lys	Glu	Phe	Glu	Pro	Thr	Leu	Ser	Arg	Gly	Gly	Asp	Met	Pro	Gln	Asp	180	185	190	
Phe	Leu	Ser	Pro	Ser	Ala	Ile	Asp	Lys	Thr	Leu	Lys	Glu	Thr	Gly	Glu	195	200	205	
Ala	Ala	Met	Lys	Ala	Ser	Leu	Ala	Lys	Arg	Met	Pro	His	Gly	Tyr	Glu	210	215	220	
Val	Gly	Tyr	Lys	Phe	Phe	Thr	Ile	Asn	Gly	Arg	Met	Leu	Gly	His	Gly	225	230	235	240
Glu	Pro	Ile	Arg	Val	Lys	His	Gly	Glu	Arg	Val	Leu	Phe	His	Ile	Leu	245	250	255	
Asn	Gly	Ser	Ala	Thr	Glu	Ile	Arg	Ser	Leu	Ala	Leu	Pro	Asp	His	Ser	260	265	270	
Phe	Glu	Val	Ile	Ala	Leu	Asp	Gly	Asn	Pro	Val	Pro	Asn	Pro	Val	His	275	280	285	
Val	Pro	Val	Leu	Trp	Leu	Gly	Thr	Ala	Glu	Arg	Ile	Ser	Ala	Val	Val	290	295	300	
Glu	Met	Asn	His	Pro	Gly	Val	Trp	Ile	Leu	Gly	Asp	Leu	Ala	Asp	Asp	305	310	315	320
Asp	Arg	Asn	His	Gly	Met	Gly	Val	Val	Val	Glu	Tyr	Ala	Gly	Arg	Ser	325	330	335	
Gly	Lys	Pro	His	Trp	Ala	Thr	Pro	Pro	Pro	Phe	Arg	Trp	Asp	Tyr	Ala	340	345	350	
Arg	Phe	Ala	Lys	Pro	Asn	Ala	Ser	Ala	Pro	Glu	Ala	Asp	Glu	Ala	Phe	355	360	365	
Asp	Met	Thr	Phe	Ala	Lys	Asp	Asn	Ala	Ala	Glu	Ala	Gly	Phe	Asn	Arg	370	375	380	
Trp	Thr	Ile	Asn	Gly	Val	Ala	Tyr	Pro	Met	Ser	Asn	Glu	Met	Ala	Pro	385	390	395	400



Ala Ser Phe His Leu Arg Gln Gly Lys Arg Tyr Arg Leu Arg Met Arg  
 405 410 415  
 Asn Ala Ser Asp Ile His Pro Ile His Leu His Arg His Ser Phe  
 420 425 430  
 Glu Leu Ala Asn Leu Ala Gly Thr Lys Thr Ala Gly Val Met Lys Asp  
 435 440 445  
 Val Val Met Leu Gly Gly Tyr Gln Gln Leu Glu Ile Asp Phe Val Ala  
 450 455 460  
 Asp Asn Pro Gly Leu Thr Leu Phe His Cys His Gln Gln Leu His Met  
 465 470 475 480  
 Asp Phe Gly Phe Met Ala Leu Phe Asp Tyr Val  
 485 490

<210> 9  
 <211> 1293  
 <212> DNA  
 <213> Unknown

<220>  
 <223> Obtained from an environmental sample

<400> 9  
 atggtgtctc gtcgaaattt tctcagcggc tccggcgccg cgttggttggg ggccggcactg 60  
 gtcagcaagg ccggcgccgc atcattgccc gaggcgccc ccatgaccac ggccgcgatg 120  
 cagccaccgc tcgtgcccc ggctggcgcg ccatacacgc ccgttgccac gttgaacggc 180  
 tggctcgtgc cgtggcgcat gaagaacggc tggaaggagt ttcatctgat tgccgagccg 240  
 gtggtgcgcg aactcgcgcc gggcatgagt gctcatctgt ggggctataa cggtcaggcg 300  
 ccggggccga ccatcgaggc cgttgaaggc gacaagggtc gcatcttcgt gaccaacagg 360  
 ctgccggagt acaccacggt tcaactggcat ggcatgctcc tgccgtgcgg catggacggc 420  
 gtcggcggtc tcacgcagcc gcatattccg ccgggcaaga cctttgttta cgagtttcag 480  
 ctcgagaagc acggcacggt catgtatcac ccgcacgcc acgagatggt gcagatggcg 540  
 atgggcatga tgggcagctt catcgttcat ccgaaggacc cgggcgtcat gcgggtggat 600  
 cgcgacttcg tggtcatcat gtccgcgtac gacatcgacc caggcagctt cacgccgcgc 660  
 gtgaacgaga tgaccgactt caacatatgg acgtggaatg cccgcgtgtt tccgggtatc 720  
 gatgcgttgc cggtcgcgcg gggcgatcgc gtgcgcattc gcgtcggcaa tctgacgatg 780  
 accaatcacc ccatccaccct gcacggctac cagttcgaag tgggtgggaac ggacggcgga 840  
 tggattcaac cctcggcgcg ctggccggag gtgaccgcgg atgtcgcggt cggccagatg 900  
 cgcgcgatcg agttcaccgc gaaccggccc ggcgactggg cgtttcattg ccacaaatcc 960  
 catcacagca tgaatcgcat ggggcaccag gtgccgaacc tgatcggcgt gccgcagcag 1020  
 gacctcgca aacgtatcaa caggctgggtg cccgattaca tggcgatggg cagcacgggc 1080  
 ggttcaatgg ggggcatgga aatgccgcta cccgataaca cgttgccgat gatggccggc 1140  
 acggggccgt tcggcgcgct ggaaatgggc ggcatgttca gcgtcgtgaa agtgcgggag 1200  
 gggttggggc gcaacgacta tcgcgacccg ggggtggttca ggcatccgca aggaaccgtg 1260  
 gcgtacgaat acaccggcga actgcctggt tga 1293

<210> 10  
 <211> 430  
 <212> PRT  
 <213> Unknown

<220>  
 <223> Obtained from an environmental sample

<221> SIGNAL  
 <222> (1)...(26)

<221> DOMAIN  
 <222> (199)...(343)  
 <223> Multicopper oxidase

&lt;400&gt; 10

```

Met Val Ser Arg Arg Asn Phe Leu Ser Gly Ser Gly Ala Ala Leu Leu
 1      5      10      15
Gly Ala Ala Leu Val Ser Lys Ala Gly Ala Ala Ser Leu Pro Glu Ala
 20      25      30
Pro Thr Met Thr Thr Ala Ala Met Gln Pro Pro Leu Val Pro Pro Ala
 35      40      45
Gly Arg Pro Tyr Thr Pro Val Ala Thr Leu Asn Gly Trp Ser Leu Pro
 50      55      60
Trp Arg Met Lys Asn Gly Trp Lys Glu Phe His Leu Ile Ala Glu Pro
 65      70      75      80
Val Val Arg Glu Leu Ala Pro Gly Met Ser Ala His Leu Trp Gly Tyr
 85      90      95
Asn Gly Gln Ala Pro Gly Pro Thr Ile Glu Ala Val Glu Gly Asp Lys
100      105      110
Val Arg Ile Phe Val Thr Asn Arg Leu Pro Glu Tyr Thr Thr Val His
115      120      125
Trp His Gly Met Leu Leu Pro Cys Gly Met Asp Gly Val Gly Gly Leu
130      135      140
Thr Gln Pro His Ile Pro Pro Gly Lys Thr Phe Val Tyr Glu Phe Gln
145      150      155      160
Leu Glu Lys His Gly Thr Phe Met Tyr His Pro His Ala Asp Glu Met
165      170      175
Val Gln Met Ala Met Gly Met Met Gly Ser Phe Ile Val His Pro Lys
180      185      190
Asp Pro Gly Val Met Arg Val Asp Arg Asp Phe Val Phe Ile Met Ser
195      200      205
Ala Tyr Asp Ile Asp Pro Gly Ser Phe Thr Pro Arg Val Asn Glu Met
210      215      220
Thr Asp Phe Asn Ile Trp Thr Trp Asn Ala Arg Val Phe Pro Gly Ile
225      230      235      240
Asp Ala Leu Pro Val Arg Ala Gly Asp Arg Val Arg Ile Arg Val Gly
245      250      255
Asn Leu Thr Met Thr Asn His Pro Ile His Leu His Gly Tyr Gln Phe
260      265      270
Glu Val Val Gly Thr Asp Gly Gly Trp Ile Gln Pro Ser Ala Arg Trp
275      280      285
Pro Glu Val Thr Ala Asp Val Ala Val Gly Gln Met Arg Ala Ile Glu
290      295      300
Phe Thr Ala Asn Arg Pro Gly Asp Trp Ala Phe His Cys His Lys Ser
305      310      315      320
His His Thr Met Asn Ala Met Gly His Gln Val Pro Asn Leu Ile Gly
325      330      335
Val Pro Gln Gln Asp Leu Ala Lys Arg Ile Asn Arg Leu Val Pro Asp
340      345      350
Tyr Met Ala Met Gly Ser Thr Gly Gly Ser Met Gly Gly Met Glu Met
355      360      365
Pro Leu Pro Asp Asn Thr Leu Pro Met Met Ala Gly Thr Gly Pro Phe
370      375      380
Gly Ala Leu Glu Met Gly Gly Met Phe Ser Val Val Lys Val Arg Glu
385      390      395      400
Gly Leu Gly Arg Asn Asp Tyr Arg Asp Pro Gly Trp Phe Arg His Pro
405      410      415
Gln Gly Thr Val Ala Tyr Glu Tyr Thr Gly Glu Leu Pro Gly
420      425      430

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&lt;210&gt; 11

&lt;211&gt; 1338

&lt;212&gt; DNA

&lt;213&gt; Unknown

&lt;220&gt;

&lt;223&gt; Obtained from an environmental sample

&lt;400&gt; 11

atgccgcgct	ctctccagta	cttcgtcgcc	ttcaccggga	tgggcaccct	cttcgccgcc	60
acgctgctgc	tggcggeget	cgccctcgga	gacggctcag	ctgcccgcag	caccgacagc	120
acccccagcc	cggcttccgc	cgagcagccc	gacgacgggc	aaccgatcgg	cgccatcgag	180
atccgtgcct	tcgacgtcgg	gttcgagccg	acgtccatca	gcgtcgagcg	accggggcgc	240
tacaccgtca	ccttcgtcaa	cgacggcggc	gccttccacg	acctggtttt	cgcggaacgc	300
accaccctcg	aggccgcccgc	gcgtgagacg	gtcagcgggc	aggtcgtcat	ccccgccgag	360
gggctgacct	acatctgctc	ggttcccggc	cacgcccagc	ccggcatgcg	cggcgaggtg	420
atggtcggcg	acgatccgca	tgctggccat	ccgccacagc	agccgctgac	tgcgaggagg	480
atgagggaca	aggatgcggc	ccgcacggcg	ctcttccctg	ccgaaacgga	gggcaagggg	540
ggcgtgccac	tcgagccgac	cgtcctcgac	gacggaacgc	tggagtggga	gctgaccgcc	600
tccgagatcg	agtgggagac	cgagcccggg	gtctggctga	attccatggc	ctacaacggc	660
atggttcccc	gtcccagact	gcgcgcccag	gtgggcccag	gggtgcgcat	catcctgcac	720
aacgagctca	gcgagccgac	caccatccac	ttccacggcc	tgctcgtgcc	gaacgcgatg	780
gacggcgtgc	ccctcatcaa	ccaggaagcg	gtactgcccg	gcgagtcatt	cacctacgag	840
ttcgagatcc	gcaatgccgg	ctcgcacatg	taccacagcc	acttcatggc	cgagcaccag	900
gtaccgatgg	gcctgctcgg	ggcattcatc	accaccgatc	cgaacgacga	ggccgatccg	960
gcggccgaca	tcgactacac	gatgatcctc	aacgacgggc	cgctcggcta	cacgatcaac	1020
ggcaagggct	tcccggccac	agagccgata	gtggccgagt	tcggccagac	gatccgcgtg	1080
cgctacatga	acgagggact	gcagatccac	ccgatgcacc	tgacacgcat	cgctcagcag	1140
gtgatcgcg	gcgacggcta	ccttgtgccg	caccgcgtact	acgaggacac	cgctcctggtt	1200
tcgcccggcg	agcgggtcga	cgtcctgata	gaggccaacg	agctcggcgt	gtgggccttc	1260
cactgccatg	tgctgaccga	cgccgagggg	ccggatggca	tgttcggaat	ggtgaccgcg	1320
ctcatcgtcc	aggagtga					1338

&lt;210&gt; 12

&lt;211&gt; 445

&lt;212&gt; PRT

&lt;213&gt; Unknown

&lt;220&gt;

&lt;223&gt; Obtained from an environmental sample

&lt;221&gt; SIGNAL

&lt;222&gt; (1)...(47)

&lt;221&gt; DOMAIN

&lt;222&gt; (322)...(445)

&lt;223&gt; Multicopper oxidase

&lt;221&gt; DOMAIN

&lt;222&gt; (55)...(143)

&lt;223&gt; Copper binding proteins, plastocyanin/azurin family

&lt;400&gt; 12

Met	Pro	Arg	Ser	Leu	Gln	Tyr	Phe	Val	Ala	Phe	Thr	Gly	Met	Gly	Thr
1				5				10					15		
Leu	Phe	Ala	Ala	Thr	Leu	Leu	Leu	Ala	Ala	Leu	Ala	Leu	Gly	Asp	Gly
			20					25					30		
Ser	Ala	Ala	Arg	Ser	Thr	Asp	Ser	Thr	Pro	Ser	Pro	Ala	Ser	Ala	Glu
			35				40					45			
Gln	Pro	Asp	Asp	Gly	Gln	Pro	Ile	Gly	Ala	Ile	Glu	Ile	Arg	Ala	Phe

50	55	60
Asp Val Gly Phe Glu Pro Thr Ser Ile Ser Val Glu Arg Pro Gly Arg		
65	70	75
Tyr Thr Val Thr Phe Val Asn Asp Gly Gly Ala Phe His Asp Leu Val		80
	85	90
Phe Ala Asp Gly Thr Thr Leu Glu Ala Ala Ala Arg Glu Thr Val Ser		95
	100	105
Gly Glu Val Val Ile Pro Ala Glu Gly Leu Thr Tyr Ile Cys Ser Val		110
	115	120
Pro Gly His Ala Asp Ala Gly Met Arg Gly Glu Val Met Val Gly Asp		125
	130	135
Asp Pro His Ala Gly His Pro Pro Gln Gln Pro Leu Thr Ala Glu Glu		140
	145	150
Met Arg Asp Lys Asp Ala Ala Arg Thr Ala Leu Phe Pro Ala Glu Thr		155
	165	170
Glu Gly Lys Gly Gly Val Pro Leu Glu Pro Thr Val Leu Asp Asp Gly		175
	180	185
Thr Leu Glu Trp Glu Leu Thr Ala Ser Glu Ile Glu Trp Glu Thr Glu		190
	195	200
Pro Gly Val Trp Leu Asn Ser Met Ala Tyr Asn Gly Met Val Pro Gly		205
	210	215
Pro Glu Leu Arg Ala Glu Val Gly Asp Arg Val Arg Ile Ile Leu His		220
	225	230
Asn Glu Leu Ser Glu Pro Thr Thr Ile His Phe His Gly Leu Leu Val		235
	245	250
Pro Asn Ala Met Asp Gly Val Pro Leu Ile Asn Gln Glu Ala Val Leu		255
	260	265
Pro Gly Glu Ser Phe Thr Tyr Glu Phe Glu Ile Arg Asn Ala Gly Ser		270
	275	280
His Met Tyr His Ser His Phe Met Ala Glu His Gln Val Pro Met Gly		285
	290	295
Leu Leu Gly Ala Phe Ile Thr Thr Asp Pro Asn Asp Glu Ala Asp Pro		300
	305	310
Ala Ala Asp Ile Asp Tyr Thr Met Ile Leu Asn Asp Gly Pro Leu Gly		315
	325	330
Tyr Thr Ile Asn Gly Lys Gly Phe Pro Ala Thr Glu Pro Ile Val Ala		335
	340	345
Glu Phe Gly Gln Thr Ile Arg Val Arg Tyr Met Asn Glu Gly Leu Gln		350
	355	360
Ile His Pro Met His Leu His Gly Ile Ala Gln Gln Val Ile Ala Arg		365
	370	375
Asp Gly Tyr Leu Val Pro His Pro Tyr Tyr Glu Asp Thr Val Leu Val		380
	385	390
Ser Pro Gly Glu Arg Val Asp Val Leu Ile Glu Ala Asn Glu Leu Gly		395
	405	410
Val Trp Ala Phe His Cys His Val Leu Thr His Ala Glu Gly Pro Asp		415
	420	425
Gly Met Phe Gly Met Val Thr Ala Leu Ile Val Gln Glu		430
	435	440
		445

&lt;210&gt; 13

&lt;211&gt; 1452

&lt;212&gt; DNA

&lt;213&gt; Bacteria

&lt;400&gt; 13

atgacggccg	cgggggccgc	cctcaccgcg	agcggactcc	tcatcagccg	gacctcgctc	60
agcgacaccc	gggcccggcg	cccggcgggc	gcctcgccgt	tcgccgccca	gccggtggcc	120
gcccgagccc	tcgccccgat	cgtcacgccc	ttccgcaccg	ccatgcccac	cccgcgggtg	180

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gcccggccgg tctccgtcac ctcgaccacc gacacgtaca gcatcccggg caccagacc 240
acggcgagaga tcatccccgg ggtccgcacc cccgtcctca cctacggcgg cagettcccc 300
ggccccacca tcaaggcgcg ctccgggtcg cgcgtgggtcg tcaagcagcc caaccggatc 360
accaccggca cctccatgca cctgcacgga gcggtcgtcg accccgccaa cgacggcggc 420
cccatggacc tgatcacgcc cggcggggcag cgcacgtaca cctaccccaa cccgcagggtg 480
gcggccaccc tctggtacca cgaccacgcc caccacatgg aggcgagca cgtctaccgc 540
ggcatgtcgg gcttctacct gatatccgac gacaacgagg acgcgctgcc cctgccgcgc 600
ggcacctacg acgtgccgat cgtcgttcgc gacatcgggc tcaaccccgga cggcacccctc 660
ttcttcgacc acaacttcga cacccgggcg cagatcctgg tcaacggcaa gccgcagccc 720
tacttcagg tcgccgcccg caagtaccgg ctgcgcatcc tcaacggctc caaccagcgg 780
cccttcgagt tccggtcttc cgacggcggc gaggttcacc agatcgctc cgaccgcggc 840
ctgctccccg ccccgtagac gacgacgacc ctgccgtctc cgccggccga acgggcccgc 900
atcgtcgtcg acttctcgcg ctaccccggtg ggcagcagcg tcgtcctgga gaacgcctac 960
ttcccgagac cctccaacaa ggagatcctc cgcttcgacg tcgtccgctc cgcctacgac 1020
cccagctcgg tcccgggccc gctcgccacc ctgccgccga ccgccgcgcc gaccagacg 1080
cgcaactaca cgctcgactt cgacgtgcag accggcgcgg gctcgatcag cggcaagacc 1140
tgggacgagc agcgcgtcga caccacggtg cgccaggggg acaccgaggt ctgggagatc 1200
aagaacaccc accccttcac cccgcacaac ttccacatcc acctggtgga cttccggtc 1260
ctcgacatcg acggcaagcc gccgacgccc ggcgacgccc gactcaagga caccgtccgg 1320
atcggggccgg gggagacggc ccgcatactc gtccacttcg acttcccgtc ctggggccgc 1380
tactactacc actgccacct gatcgaccac tcgtcgatgg gcatgatggc caacctggag 1440
atcacccgat ga 1452

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&lt;210&gt; 14

&lt;211&gt; 483

&lt;212&gt; PRT

&lt;213&gt; Bacteria

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; (1) ... (21)

&lt;400&gt; 14

```

Met Thr Ala Ala Gly Ala Ala Leu Thr Ala Ser Gly Leu Leu Ile Ser
 1          5          10          15
Arg Thr Ser Leu Ser Asp Thr Arg Ala Gly Gly Pro Ala Gly Ala Ser
 20          25          30
Pro Phe Ala Ala Gln Pro Val Ala Ala Gln Ala Leu Ala Pro Ile Val
 35          40          45
Thr Pro Phe Arg Thr Ala Met Pro Ile Pro Pro Val Ala Arg Pro Val
 50          55          60
Ser Val Thr Ser Thr Thr Asp Thr Tyr Ser Ile Pro Val Thr Gln Thr
 65          70          75          80
Thr Ala Glu Ile Ile Pro Gly Val Arg Thr Pro Val Leu Thr Tyr Gly
 85          90          95
Gly Ser Phe Pro Gly Pro Thr Ile Lys Ala Arg Ser Gly Arg Arg Val
 100         105         110
Val Val Lys Gln Pro Asn Arg Ile Thr Thr Gly Thr Ser Met His Leu
 115         120         125
His Gly Ala Val Val Asp Pro Ala Asn Asp Gly Gly Pro Met Asp Leu
 130         135         140
Ile Thr Pro Gly Gly Gln Arg Thr Tyr Thr Tyr Pro Asn Pro Gln Val
 145         150         155         160
Ala Ala Thr Leu Trp Tyr His Asp His Ala His His Met Glu Ala Glu
 165         170         175
His Val Tyr Arg Gly Met Ser Gly Phe Tyr Leu Ile Ser Asp Asp Asn
 180         185         190
Glu Asp Ala Leu Pro Leu Pro Arg Gly Thr Tyr Asp Val Pro Ile Val
 195         200         205

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Val Arg Asp Ile Gly Leu Asn Pro Asp Gly Thr Leu Phe Phe Asp His  
 210 215 220  
 Asn Phe Asp Thr Arg Pro Gln Ile Leu Val Asn Gly Lys Pro Gln Pro  
 225 230 235 240  
 Tyr Phe Gln Val Ala Ala Arg Lys Tyr Arg Leu Arg Ile Leu Asn Gly  
 245 250 255  
 Ser Asn Gln Arg Pro Phe Glu Phe Arg Leu Ser Asp Gly Gly Glu Phe  
 260 265 270  
 Thr Gln Ile Ala Ser Asp Arg Gly Leu Leu Pro Ala Pro Tyr Thr Thr  
 275 280 285  
 Thr Thr Leu Pro Leu Ser Pro Ala Glu Arg Ala Asp Ile Val Val Asp  
 290 295 300  
 Phe Ser Arg Tyr Pro Val Gly Ser Ser Val Val Leu Glu Asn Ala Tyr  
 305 310 315 320  
 Phe Pro Glu Pro Ser Asn Lys Glu Ile Leu Arg Phe Asp Val Val Arg  
 325 330 335  
 Ser Ala Tyr Asp Pro Ser Ser Val Pro Ala Arg Leu Ala Thr Leu Pro  
 340 345 350  
 Pro Thr Ala Ala Pro Thr Gln Thr Arg Asn Tyr Thr Leu Asp Phe Asp  
 355 360 365  
 Val Gln Thr Gly Ala Gly Ser Ile Ser Gly Lys Thr Trp Asp Glu Gln  
 370 375 380  
 Arg Val Asp Thr Thr Val Arg Gln Gly Asp Thr Glu Val Trp Glu Ile  
 385 390 395 400  
 Lys Asn Thr His Pro Phe Ile Pro His Asn Phe His Ile His Leu Val  
 405 410 415  
 Asp Phe Arg Ile Leu Asp Ile Asp Gly Lys Pro Pro Thr Pro Gly Asp  
 420 425 430  
 Ala Gly Leu Lys Asp Thr Val Arg Ile Gly Pro Gly Glu Thr Ala Arg  
 435 440 445  
 Ile Leu Val His Phe Asp Phe Pro Tyr Ser Gly Arg Tyr Tyr Tyr His  
 450 455 460  
 Cys His Leu Ile Asp His Ser Ser Met Gly Met Met Ala Asn Leu Glu  
 465 470 475 480  
 Ile Thr Arg

&lt;210&gt; 15

&lt;211&gt; 1542

&lt;212&gt; DNA

&lt;213&gt; Unknown

&lt;220&gt;

&lt;223&gt; Obtained from an environmental sample

&lt;400&gt; 15

atgacacttg	aaaaatttgt	ggatgctctc	ccaatcccag	atacactaaa	gccggtacag	60
cagtcaaaaag	atagcacata	ctacgaagta	accatggagg	aatgctacca	tcagcttcac	120
cgcgatctcc	ctccaacccg	cttgtggggc	tataacgggt	tattccccgg	tcccaccatt	180
aaggccaaaa	gaaatgaaaa	cgtttatgtg	aagtggatga	ataaccttcc	ttcagagcat	240
tttcttccga	ttgatcacac	cattcatcac	agtgcagcc	agcatgccga	acccgaggtg	300
aaaaccgtcg	ttcatttaca	cggcggcgctc	actccagatg	acagcgacgg	ttatcctgag	360
gcctggtttt	ctaaagactt	tgaacaaaca	ggcccttatt	ttaaacgaga	ggtttaccat	420
tatccaaatc	agcagcgcg	agctatttta	tggtatcacg	atcatgctat	ggcgctcacg	480
aggctgaatg	tgtatgccgg	gctcatcggt	gcttatatca	tccatgaacc	aaaggaaaaa	540
cgctgaagc	tcccatcagg	tgaatacga	gtgccgcttt	tgatcacgga	ccgtacgatt	600
aatgaagatg	gctctttatt	ttatccgagc	ggaccggaaa	acccttcacc	gtcactgcct	660
aatccgtaaa	tcgttccagc	cttttgcgga	gatacaattc	tcgtcaacgg	gaaggcatgg	720
ccatacatgg	aggtcgaacc	gagaaaatac	cgcttccgcg	tcataaatgc	ctctaatacg	780

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agaacatata acctgtcact tgataatggt ggagaattta tccagatcgg ttctgacggc      840
ggacttttgc cgcgctccgt catgctaaac tctttcagta tcgcgccagc tgagcgcttt      900
gatatcctca ttgacttcgc cgcggttgaa ggacaatcga ttatttttagc aaacagcgag      960
ggctgcggcg gcgacgttaa tccggaaaca gacgcaaaca tcatgcaatt cagagtcaca     1020
aaaccgttag cccaaaaaga cgaaagcaga aagccaaaat acctggcatc ttacccttca     1080
gtacagcacg aaagaatata aaacctccga acattgaagc tggcaggaac tcaagatcaa     1140
tacggcagac ccgttcttct tcttaacaac aaacgctggc acgatcctgt cactgaagca     1200
ccgaaagccg gttctaccga aatatggctg atcatcaatc cgacacgcgg aacacatccc     1260
atccatcttc atttggcttc cttccgtgta ttggaccggc gccatttga tacagcccgt     1320
tttgaagagc gcggagaact ggcctacacc ggaccgcggc ttccgcccgc accaagtga     1380
aaaggctgga aagacacggg tcagtcccac gccggtgaag tcctgagaat cgccgtaaca     1440
ttcgggccat acactgggcg gtacgtatgg cattgccaca ttcttgagca tgaagactat     1500
gacatgatga gaccgatgga tgtgattgac ccccataaat aa                        1542

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<210> 16

<211> 513

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 16

```

Met Thr Leu Glu Lys Phe Val Asp Ala Leu Pro Ile Pro Asp Thr Leu
1          5          10          15
Lys Pro Val Gln Gln Ser Lys Asp Ser Thr Tyr Tyr Glu Val Thr Met
20          25          30
Glu Glu Cys Tyr His Gln Leu His Arg Asp Leu Pro Pro Thr Arg Leu
35          40          45
Trp Gly Tyr Asn Gly Leu Phe Pro Gly Pro Thr Ile Lys Ala Lys Arg
50          55          60
Asn Glu Asn Val Tyr Val Lys Trp Met Asn Asn Leu Pro Ser Glu His
65          70          75          80
Phe Leu Pro Ile Asp His Thr Ile His His Ser Asp Ser Gln His Ala
85          90          95
Glu Pro Glu Val Lys Thr Val Val His Leu His Gly Gly Val Thr Pro
100          105          110
Asp Asp Ser Asp Gly Tyr Pro Glu Ala Trp Phe Ser Lys Asp Phe Glu
115          120          125
Gln Thr Gly Pro Tyr Phe Lys Arg Glu Val Tyr His Tyr Pro Asn Gln
130          135          140
Gln Arg Gly Ala Ile Leu Trp Tyr His Asp His Ala Met Ala Leu Thr
145          150          155          160
Arg Leu Asn Val Tyr Ala Gly Leu Ile Gly Ala Tyr Ile Ile His Glu
165          170          175
Pro Lys Glu Lys Arg Leu Lys Leu Pro Ser Gly Glu Tyr Asp Val Pro
180          185          190
Leu Leu Ile Thr Asp Arg Thr Ile Asn Glu Asp Gly Ser Leu Phe Tyr
195          200          205
Pro Ser Gly Pro Glu Asn Pro Ser Pro Ser Leu Pro Asn Pro Ser Ile
210          215          220
Val Pro Ala Phe Cys Gly Asp Thr Ile Leu Val Asn Gly Lys Ala Trp
225          230          235          240
Pro Tyr Met Glu Val Glu Pro Arg Lys Tyr Arg Phe Arg Val Ile Asn
245          250          255
Ala Ser Asn Thr Arg Thr Tyr Asn Leu Ser Leu Asp Asn Gly Gly Glu
260          265          270
Phe Ile Gln Ile Gly Ser Asp Gly Gly Leu Leu Pro Arg Ser Val Met
275          280          285

```

Leu Asn Ser Phe Ser Ile Ala Pro Ala Glu Arg Phe Asp Ile Leu Ile  
 290 295 300  
 Asp Phe Ala Ala Phe Glu Gly Gln Ser Ile Ile Leu Ala Asn Ser Glu  
 305 310 315 320  
 Gly Cys Gly Gly Asp Val Asn Pro Glu Thr Asp Ala Asn Ile Met Gln  
 325 330 335  
 Phe Arg Val Thr Lys Pro Leu Ala Gln Lys Asp Glu Ser Arg Lys Pro  
 340 345 350  
 Lys Tyr Leu Ala Ser Tyr Pro Ser Val Gln His Glu Arg Ile Gln Asn  
 355 360 365  
 Leu Arg Thr Leu Lys Leu Ala Gly Thr Gln Asp Gln Tyr Gly Arg Pro  
 370 375 380  
 Val Leu Leu Leu Asn Asn Lys Arg Trp His Asp Pro Val Thr Glu Ala  
 385 390 395 400  
 Pro Lys Ala Gly Ser Thr Glu Ile Trp Ser Ile Ile Asn Pro Thr Arg  
 405 410 415  
 Gly Thr His Pro Ile His Leu His Leu Val Ser Phe Arg Val Leu Asp  
 420 425 430  
 Arg Arg Pro Phe Asp Thr Ala Arg Phe Glu Glu Arg Gly Glu Leu Ala  
 435 440 445  
 Tyr Thr Gly Pro Ala Val Pro Pro Pro Pro Ser Glu Lys Gly Trp Lys  
 450 455 460  
 Asp Thr Val Gln Ser His Ala Gly Glu Val Leu Arg Ile Ala Val Thr  
 465 470 475 480  
 Phe Gly Pro Tyr Thr Gly Arg Tyr Val Trp His Cys His Ile Leu Glu  
 485 490 495  
 His Glu Asp Tyr Asp Met Met Arg Pro Met Asp Val Ile Asp Pro His  
 500 505 510  
 Lys

<210> 17  
 <211> 1743  
 <212> DNA  
 <213> Unknown

<220>  
 <223> Obtained from an environmental sample

<400> 17  
 ttggatgttg gcgggccggt cgactattac gagatcgcgg tgcgccagtt tcaacagcag 60  
 atattgcctc cacctttacc ggccacaact gtgtggagtt atggctcgac gaaccattcc 120  
 ggcactttta attatccggc ttccaccatc gaagccaaat ggaacacacc tgtgcgcgtg 180  
 aagtggatca acgatctgaa agatctatcg agcggcgaat tcttaccgca cttgctgccc 240  
 gttgatccga ctcttactg ggcgaatccg ccaggaggtc ttggcggccg tgacatgcgt 300  
 cccgaattca caactactcc agatccatat agaggaccg tgccgatcgt cacgcatctg 360  
 cacggcggac acaccagcca ggagagcgat ggctttacag aagcgtggta tctgccgacc 420  
 gcaaccaata tccccgctgg attcgcgact gaaggtacct ggtacgatac tttcaaaaca 480  
 caattttctca accagtgggg tgtgccctgg cagccaggct ctgcgatctt tcaatatgcc 540  
 aacgaccagc gagcgagcac gctctggtat catgatcacg cgctcggcat gacgcgtttg 600  
 aatgtctatg ccggaccggc ggggttttac ttgttgccgc gtgggcccaga cgatatggtt 660  
 gtgggcactc tgcctggacc cgctcccgcg ttagacgatc cgagtggcat gaagtactac 720  
 gagatccccc tcgcaatcca ggatcgctca ttcaacaaaag atggttcctt gttctatccg 780  
 gagagccggc gattctttga cggctttaag aaggcataca ttcccagacag cgacatctcc 840  
 ccaatatgga atccggaatt ctccggcaaa gtaatgggtg tcaacggccg cagctggccc 900  
 ttccttgaag ttgagccgcg ccgctatcgt ttccggctgc tgaatggatg caactctcgt 960  
 ttcctgatcc tgaagttcag caatccgaat ttaagcttct ggcagattgg taatgacggc 1020  
 gggttcttgc cggcgccagt gcaactctcg caactgctga tgtcgccggc agaacgggca 1080  
 gatgtgatcg tagacttttc gcaattcacg ccaggcaccg aaatcatttt ggagaacact 1140



```

ggtcctgatg agccgttcgg tgggggagcg ccagacagcg atttcgacag cgccaaggcg 1200
gacacaacgc ggcaggtgat gcaattcagg gtcgtgccgc tgacaacagc ggataacaagc 1260
acaccaccta atctcctcga gttgccggcg atcactgggtt tgggtgcagc aaccaacacg 1320
cggcaggttt cgctcaacga agaggactca gcagtgcgtg tcggtgtcgg accaagagct 1380
gcgctgcttg gtactctgga tagtgagggc gagccggaga ttagaggctg ggacgatgcg 1440
atcactgaaa acccggccct tggcagcatc gaggtatggg agattcaciaa cttcacagaa 1500
gacgcgcacc cgattcacat tcacgaggtg gcgtttgaag tggatcaatcg acagccgttc 1560
gagggatctg caagaggtcc ggaagtttgg gaaggaggat tcaaggatac agtgatcgca 1620
tatccggagg agatcacgcg cgtcaaggct catttcgatc tgccgggact atatgtttgg 1680
cactgtcaca tcgtggagca cgaggacaac gaaatgatgc gcccctactt cattggccccg 1740
tga

```

&lt;210&gt; 18

&lt;211&gt; 580

&lt;212&gt; PRT

&lt;213&gt; Unknown

&lt;220&gt;

&lt;223&gt; Obtained from an environmental sample

&lt;400&gt; 18

```

Met Asp Val Gly Gly Pro Val Asp Tyr Tyr Glu Ile Ala Val Arg Gln
 1          5          10          15
Phe Gln Gln Gln Ile Leu Pro Pro Pro Leu Pro Ala Thr Thr Val Trp
 20          25          30
Ser Tyr Gly Ser Thr Asn His Ser Gly Thr Phe Asn Tyr Pro Ala Phe
 35          40          45
Thr Ile Glu Ala Lys Trp Asn Thr Pro Val Arg Val Lys Trp Ile Asn
 50          55          60
Asp Leu Lys Asp Leu Ser Ser Gly Glu Phe Leu Pro His Leu Leu Pro
 65          70          75          80
Val Asp Pro Thr Leu His Trp Ala Asn Pro Pro Gly Gly Leu Gly Gly
 85          90          95
Arg Asp Met Arg Pro Glu Phe Thr Thr Thr Pro Asp Pro Tyr Arg Gly
100          105          110
Pro Val Pro Ile Val Thr His Leu His Gly Gly His Thr Ser Gln Glu
115          120          125
Ser Asp Gly Phe Thr Glu Ala Trp Tyr Leu Pro Thr Ala Thr Asn Ile
130          135          140
Pro Ala Gly Phe Ala Thr Glu Gly Thr Trp Tyr Asp Thr Phe Lys Thr
145          150          155          160
Gln Phe Leu Asn Gln Trp Gly Val Pro Trp Gln Pro Gly Ser Ala Ile
165          170          175
Phe Gln Tyr Ala Asn Asp Gln Arg Ala Ser Thr Leu Trp Tyr His Asp
180          185          190
His Ala Leu Gly Met Thr Arg Leu Asn Val Tyr Ala Gly Pro Ala Gly
195          200          205
Phe Tyr Leu Leu Arg Gly Gly Pro Asp Asp Met Val Val Gly Thr Leu
210          215          220
Pro Gly Pro Ala Pro Ala Leu Asp Asp Pro Ser Gly Met Lys Tyr Tyr
225          230          235          240
Glu Ile Pro Leu Ala Ile Gln Asp Arg Ser Phe Asn Lys Asp Gly Ser
245          250          255
Leu Phe Tyr Pro Asp Ser Arg Arg Phe Phe Asp Gly Phe Lys Lys Ala
260          265          270
Tyr Ile Pro Asp Ser Asp Ile Ser Pro Ile Trp Asn Pro Glu Phe Phe
275          280          285
Gly Lys Val Met Val Val Asn Gly Arg Ser Trp Pro Phe Leu Glu Val
290          295          300

```

Glu Pro Arg Arg Tyr Arg Phe Arg Leu Leu Asn Gly Cys Asn Ser Arg  
 305 310 315 320  
 Phe Leu Ile Leu Lys Phe Ser Asn Pro Asn Leu Ser Phe Trp Gln Ile  
 325 330 335  
 Gly Asn Asp Gly Gly Phe Leu Pro Ala Pro Val Gln Leu Ser Gln Leu  
 340 345 350  
 Leu Met Ser Pro Ala Glu Arg Ala Asp Val Ile Val Asp Phe Ser Gln  
 355 360 365  
 Phe Thr Pro Gly Thr Glu Ile Ile Leu Glu Asn Thr Gly Pro Asp Glu  
 370 375 380  
 Pro Phe Gly Gly Gly Glu Pro Asp Ser Asp Phe Asp Ser Ala Lys Ala  
 385 390 395 400  
 Asp Thr Thr Arg Gln Val Met Gln Phe Arg Val Val Pro Leu Thr Thr  
 405 410 415  
 Ala Asp Thr Ser Thr Pro Pro Asn Leu Leu Glu Leu Pro Ala Ile Thr  
 420 425 430  
 Gly Leu Gly Ala Ala Thr Asn Thr Arg Gln Val Ser Leu Asn Glu Glu  
 435 440 445  
 Asp Ser Ala Val Leu Phe Gly Val Gly Pro Arg Ala Ala Leu Leu Gly  
 450 455 460  
 Thr Leu Asp Ser Glu Gly Glu Pro Glu Ile Arg Gly Trp Asp Asp Ala  
 465 470 475 480  
 Ile Thr Glu Asn Pro Ala Leu Gly Ser Ile Glu Val Trp Glu Ile His  
 485 490 495  
 Asn Phe Thr Glu Asp Ala His Pro Ile His Ile His Glu Val Ala Phe  
 500 505 510  
 Glu Val Val Asn Arg Gln Pro Phe Glu Gly Ser Ala Arg Gly Pro Glu  
 515 520 525  
 Val Trp Glu Gly Gly Phe Lys Asp Thr Val Ile Ala Tyr Pro Glu Glu  
 530 535 540  
 Ile Thr Arg Val Lys Ala His Phe Asp Leu Pro Gly Leu Tyr Val Trp  
 545 550 555 560  
 His Cys His Ile Val Glu His Glu Asp Asn Glu Met Met Arg Pro Tyr  
 565 570 575  
 Phe Ile Gly Pro  
 580

&lt;210&gt; 19

&lt;211&gt; 1467

&lt;212&gt; DNA

&lt;213&gt; Unknown

&lt;220&gt;

&lt;223&gt; Obtained from an environmental sample

&lt;400&gt; 19

atgacgaccc	gccgggattt	cctcaaacgg	gccggcctgg	gcctcgccgc	agccgccacg	60
ctgcccgtgc	tttcaggctg	tccggacgcg	ttgttcggtt	acggcgctcg	cacacgtcgc	120
tccgccgacg	gactttctga	caccgggctt	cggctgcgtt	tcagtcatac	ctgtatcggc	180
cacgaacagg	tttacacccg	cgcctacgac	ggccgtatcc	caggacccgt	gctccgcgtg	240
aaaccgggcg	acaccctcaa	gatccgcctg	atcaacgatt	tgccggatga	ggaggacggc	300
cacggccacg	caaagtccga	tgacgtcaac	gtccctcatg	gattcaatac	caccaacatc	360
cacacccacg	ggttgacagt	ctcgccgtct	ggcaattccg	acaatgtctt	cgtccagatt	420
ccgcccgga	cgcatttcga	ttacgaatac	aacatcccgg	cgaatcatcc	cgcaggaaca	480
tttttctacc	atccgcacaa	gcacggttcg	gtcaccaacc	agatgatggg	tggtatggcc	540
ggtgcgctga	ttgtcgaggg	agacatcgac	cgcgtaccgg	agatcgctgc	cgcgaaggac	600
tatatcttcc	tgttacagga	actgcgcttc	gaggaggacg	gccacgcgcc	ggcgcathtt	660
ccgttccacg	atcttgacaa	cctgatgttg	ttccgcacgg	tgaacgggca	ggtcaacccc	720
acgatttacc	ttcggccccg	cgaggtgcag	cgctggcgat	tcattccatgc	gggcgtcgaa	780

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cactatctgc ccctcgaatt ggatggacat tgcgtccacc aaatcgcgca ggacggcatc      840
gccttcgct  cgccgaaga gacggacagc gtctttctca cccccggcaa ccgtgctgac      900
gtactcgtgc gcggtggcca acccggcacg tattacctgc gcaaacaggc ctatgaccag      960
ggacgcggcg aggtccccga agacattatc gccaccgtcg tcgtgaccgg gccgccttcc     1020
tttatgcgcc ttccctggct gctgccgacg cctgcgctgc accgcaccat tactgacgaa     1080
gaagtgaccg gttcgcgcag tatcgtcttt agtgtgcaac ccgcgccagc gggcgaaatg     1140
tttcgcgcgt ttctgattga cgggcatact ttttcgccgg accgggtcga tcactctatt     1200
ccgctcggtt ccgtcgagga atggacggtt atcaacaacc accgggaaga ccatcccttc     1260
cacatccacg tcaatgcctt tgaagtcacc cacctgaacg gtgaccggct cccgcgcca     1320
cgctggcacg atgtaatcaa cgtgcccccc ttcggcactg cgaccttccg taccgcttc     1380
gaagatttca cgggcaagtt cgtcctgcac tgccacctcc tcgtccacga agacctcggc     1440
atgatgcaga cggttgaagt cacctga                                     1467

```

<210> 20

<211> 488

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<221> SIGNAL

<222> (1)...(25)

<221> DOMAIN

<222> (201)...(339)

<223> Multicopper oxidase

<400> 20

```

Met Thr Thr Arg Arg Asp Phe Leu Lys Arg Ala Gly Leu Gly Leu Ala
 1                    5          10          15
Ala Ala Ala Thr Leu Pro Val Leu Ser Gly Cys Pro Asp Ala Leu Phe
                20          25          30
Arg Tyr Gly Val Ala Thr Arg Arg Ser Ala Asp Gly Leu Leu Asp Thr
                35          40          45
Arg Leu Arg Leu Arg Phe Ser His Thr Cys Ile Gly His Glu Gln Val
 50          55          60
Tyr Thr Arg Ala Tyr Asp Gly Arg Ile Pro Gly Pro Val Leu Arg Val
 65          70          75          80
Lys Pro Gly Asp Thr Leu Lys Ile Arg Leu Ile Asn Asp Leu Pro Asp
                85          90          95
Glu Glu Asp Gly His Gly His Ala Lys Ser Asp Asp Val Asn Val Pro
                100          105          110
His Gly Phe Asn Thr Thr Asn Ile His Thr His Gly Leu His Val Ser
                115          120          125
Pro Ser Gly Asn Ser Asp Asn Val Phe Val Gln Ile Pro Pro Gly Thr
                130          135          140
His Phe Asp Tyr Glu Tyr Asn Ile Pro Ala Asn His Pro Ala Gly Thr
 145          150          155          160
Phe Phe Tyr His Pro His Lys His Gly Ser Val Thr Asn Gln Met Met
                165          170          175
Gly Gly Met Ala Gly Ala Leu Ile Val Glu Gly Asp Ile Asp Arg Val
                180          185          190
Pro Glu Ile Ala Ala Ala Lys Asp Tyr Ile Phe Leu Leu Gln Glu Leu
                195          200          205
Arg Phe Glu Glu Asp Gly His Ala Pro Ala His Phe Pro Phe His Asp
 210          215          220
Leu Asp Asn Leu Met Leu Phe Arg Thr Val Asn Gly Gln Val Asn Pro
 225          230          235          240

```

Thr Ile Tyr Leu Arg Pro Gly Glu Val Gln Arg Trp Arg Phe Ile His  
 245 250 255  
 Ala Gly Val Glu His Tyr Leu Pro Leu Glu Leu Asp Gly His Ser Leu  
 260 265 270  
 His Gln Ile Ala Gln Asp Gly Ile Ala Phe Arg Ser Pro Glu Glu Thr  
 275 280 285  
 Asp Ser Val Phe Leu Thr Pro Gly Asn Arg Ala Asp Val Leu Val Arg  
 290 295 300  
 Gly Gly Gln Pro Gly Thr Tyr Tyr Leu Arg Lys Gln Ala Tyr Asp Gln  
 305 310 315 320  
 Gly Arg Gly Glu Val Pro Glu Asp Ile Ile Ala Thr Val Val Val Thr  
 325 330 335  
 Gly Pro Pro Ser Phe Met Arg Leu Pro Trp Leu Leu Pro Thr Pro Ala  
 340 345 350  
 Leu His Arg Thr Ile Thr Asp Glu Val Thr Gly Ser Arg Ser Ile  
 355 360 365  
 Val Phe Ser Val Gln Pro Ala Pro Ala Gly Glu Met Phe Pro Arg Phe  
 370 375 380  
 Leu Ile Asp Gly His Thr Phe Ser Pro Asp Arg Val Asp His Ser Ile  
 385 390 395 400  
 Pro Leu Gly Ser Val Glu Glu Trp Thr Val Ile Asn Asn His Arg Glu  
 405 410 415  
 Asp His Pro Phe His Ile His Val Asn Ala Phe Glu Val Thr His Leu  
 420 425 430  
 Asn Gly Asp Arg Leu Pro Arg Pro Arg Trp His Asp Val Ile Asn Val  
 435 440 445  
 Pro Pro Phe Gly Thr Ala Thr Phe Arg Thr Arg Phe Glu Asp Phe Thr  
 450 455 460  
 Gly Lys Phe Val Leu His Cys His Leu Leu Val His Glu Asp Leu Gly  
 465 470 475 480  
 Met Met Gln Thr Val Glu Val Thr  
 485

&lt;210&gt; 21

&lt;211&gt; 1356

&lt;212&gt; DNA

&lt;213&gt; Unknown

&lt;220&gt;

&lt;223&gt; Obtained from an environmental sample

&lt;400&gt; 21

ttgaattctt	tggatcagcc	cggcgatcgt	ggcggaggtag	aacagcagcg	ccgcggcccg	60
gtcggccagt	gcctgtgccc	gggaccggga	ggcctgagct	tgctcgacaa	ggcgacgaat	120
tccggccaac	gccgtctggt	cgccgacggc	gtcgaccctg	acccgcagtg	ccgagtcgtg	180
gccacggtgc	ccgccaccac	tcggtttcca	gcagccttgg	gcaccggccg	ggactcacca	240
gtgatcagcg	ggctcgccga	tgtcaccaat	ctccacactc	acggctttca	tgtttcaccg	300
caagggaact	ccgacaacat	cttcctccac	atcaaccccg	gcgagacctt	cgactacgag	360
ttcaagctgc	ccgcgaacca	ctcaccgggg	atgtactggt	atcaccgcga	tggtcacggc	420
gacaccgccc	cccagtgcaa	cggcggcatg	gccgggggtga	tcctgatcga	cggcggtctc	480
gacgaggtgc	cgggaatcgc	cggctctgacc	gaacgcctgc	tcgtcctcca	ggcgacgcaa	540
ttcgacggcg	acggcaacct	cgtccccttac	aacaaccagt	cgaacgcgac	tcggcagcgc	600
ttcgtcaacg	gtcaactcaa	cccaacgata	gcgattcgac	ccggcgagac	acagcgctgg	660
cggatcgcca	acgtcagctc	tgacaacttc	ttcctgctgg	cgctagctgg	tcacacgctg	720
caccagatcg	ccgcggacgg	caaccctgat	gacgaggtcg	ttccgcgcga	ccagatcctc	780
ctcccaccct	cggagcgggt	cgaggtcttg	gtgcaggcat	cgacccaact	gggaagctac	840
gagttccgca	ccctcctctg	ggcgacgat	ttccaggccg	aaccgcagct	ggtgctggcg	900
acgatggtcg	tcgctggcga	ggcaatcact	ccagcaccgc	tcccaaccgc	gctcatcccc	960
tacgaggact	tgcgggatgt	cccggctcgac	aacatccgcg	tgaccacctt	cgaggaaccg	1020

```

ggcgctcccc tctacctggc gatcgacggc aagcacttcg accccgaccg cgtcgaccag 1080
acgggtgaagt tggggggcgac ggaggagtgg atcgtccgca ataccagctc cgaatggcac 1140
ccgttccaca tccacgtcaa cgacttccag gtgatcgccg tcaacaacga agcgggtcaac 1200
acccatggct acgaggactc cgtcgccctc ccaccacaca gcgaaacgac gatgcggatg 1260
aaattcctcg acttcagcgg caaattcgtc taccactgcc acatcctcgg gcacgaagac 1320
ttcggcatga tggcggtagt ggaggtggtt gagtag 1356

```

&lt;210&gt; 22

&lt;211&gt; 451

&lt;212&gt; PRT

&lt;213&gt; Unknown

&lt;220&gt;

&lt;223&gt; Obtained from an environmental sample

&lt;400&gt; 22

```

Met Asn Ser Leu Asp Gln Pro Gly Asp Arg Gly Glu Val Glu Gln Gln
1          5          10          15
Arg Arg Gly Pro Val Gly Gln Cys Leu Cys Pro Gly Pro Gly Gly Leu
20          25          30
Ser Leu Leu Asp Lys Ala Thr Asn Ser Gly Gln Arg Arg Leu Val Ala
35          40          45
Asp Gly Val Asp Pro Tyr Pro Gln Cys Arg Val Val Ala Thr Val Pro
50          55          60
Ala Thr Thr Arg Phe Pro Ala Ala Leu Gly Thr Gly Arg Asp Ser Pro
65          70          75          80
Val Ile Ser Gly Leu Ala Asp Val Thr Asn Leu His Thr His Gly Phe
85          90          95
His Val Ser Pro Gln Gly Asn Ser Asp Asn Ile Phe Leu His Ile Asn
100         105         110
Pro Gly Glu Thr Phe Asp Tyr Glu Phe Lys Leu Pro Ala Asn His Ser
115         120         125
Pro Gly Met Tyr Trp Tyr His Pro His Gly His Gly Asp Thr Ala Pro
130         135         140
Gln Cys Asn Gly Gly Met Ala Gly Val Ile Leu Ile Asp Gly Gly Leu
145         150         155         160
Asp Glu Val Pro Gly Ile Ala Gly Leu Thr Glu Arg Leu Leu Val Leu
165         170         175
Gln Ala Thr Gln Phe Asp Gly Asp Gly Asn Leu Val Pro Tyr Asn Asn
180         185         190
Gln Ser Asn Ala Thr Arg Gln Arg Phe Val Asn Gly Gln Leu Asn Pro
195         200         205
Thr Ile Ala Ile Arg Pro Gly Glu Thr Gln Arg Trp Arg Ile Ala Asn
210         215         220
Val Ser Ser Asp Asn Phe Leu Leu Ala Leu Ala Gly His Thr Leu
225         230         235         240
His Gln Ile Ala Ala Asp Gly Asn Pro Tyr Asp Glu Val Val Pro Arg
245         250         255
Asp Gln Ile Leu Leu Pro Pro Ser Glu Arg Val Glu Val Leu Val Gln
260         265         270
Ala Ser Thr Gln Leu Gly Ser Tyr Glu Phe Arg Thr Leu Leu Trp Gly
275         280         285
Asp Asp Phe Gln Ala Glu Pro Asp Val Val Leu Ala Thr Met Val Val
290         295         300
Ala Gly Glu Ala Ile Thr Pro Ala Pro Leu Pro Thr Ala Leu Ile Pro
305         310         315         320
Tyr Glu Asp Leu Arg Asp Val Pro Val Asp Asn Ile Arg Val Thr Thr
325         330         335
Phe Glu Glu Pro Gly Ala Pro Leu Tyr Leu Ala Ile Asp Gly Lys His

```

```
<210> 24
<211> 589
<212> PRT
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<213> Unknown

<220>

<223> Obtained from an environmental sample

<221> SIGNAL

<222> (1)...(20)

<221> DOMAIN

<222> (197)...(352)

<223> Multicopper oxidase

<221> DOMAIN

<222> (390)...(556)

<223> Multicopper oxidase

<221> DOMAIN

<222> (59)...(194)

<223> Multicopper oxidase

<400> 24

Met	Lys	Ser	Phe	Ile	Gly	Thr	Val	Gly	Gly	Ile	Ala	Leu	Thr	Ala	Lys	1	5	10	15
Ala	Val	Ser	Ala	Thr	Pro	Met	Leu	Phe	Asn	Glu	Pro	Ser	Thr	Asn	Val	20	25	30	
Ala	Lys	Arg	Ala	Ala	Thr	Ser	Cys	Asn	Thr	Ala	Ser	Asn	Arg	Ser	Cys	35	40	45	
Trp	Thr	Thr	Asp	Gly	Tyr	Thr	Ile	Asp	Thr	Asn	Tyr	Val	Val	Asp	Tyr	50	55	60	
Pro	Thr	Thr	Gly	Val	Thr	Arg	Gln	Tyr	Thr	Leu	Tyr	Val	Thr	Glu	Val	65	70	75	80
Glu	Asn	Ala	Asn	Leu	Asp	Gly	Thr	Val	Lys	Asn	Ile	Ser	Met	Leu	Ile	85	90	95	
Asn	Gly	Thr	Tyr	Pro	Gly	Pro	Thr	Leu	Tyr	Ala	Asp	Trp	Gly	Asp	Asp	100	105	110	
Ile	Glu	Ile	Thr	Val	Ile	Asn	Asn	Leu	Thr	Thr	Asn	Gly	Thr	Ser	Met	115	120	125	
His	Trp	His	Gly	Val	Thr	Gln	Leu	Asn	Thr	Asn	Ile	Met	Asp	Gly	Val	130	135	140	
Asn	Gly	Val	Thr	Glu	Cys	Pro	Thr	Thr	Pro	Gly	Asp	Ser	His	Thr	Tyr	145	150	155	160
Lys	Phe	His	Val	Thr	Gln	Tyr	Gly	Ser	Thr	Trp	Tyr	His	Ser	His	Tyr	165	170	175	
Ser	Thr	Gln	Tyr	Gly	Asn	Gly	Ala	Trp	Gly	Thr	Met	Ile	Phe	Asn	Gly	180	185	190	
Pro	Ala	Ser	Ala	Asn	Tyr	Asp	Ile	Asp	Leu	Gly	Thr	Tyr	Pro	Ile	Ser	195	200	205	
Asp	Tyr	Ile	Tyr	Ala	Thr	Ala	Glu	Ala	Val	Tyr	Ala	Glu	Tyr	Val	Ile	210	215	220	
Pro	Ser	Pro	Gly	Val	Ala	Pro	Ser	Pro	Asn	Asn	Ile	Leu	Phe	Asn	Gly	225	230	235	240
Ser	His	Val	Asn	Val	Asp	Gly	Glu	Gly	Ser	Tyr	Asn	Val	Val	Thr	Leu	245	250	255	
Thr	Lys	Gly	Lys	Thr	His	Arg	Leu	Arg	Leu	Ile	Asn	Thr	Ala	Ile	Asp	260	265	270	
Ala	Glu	Met	Ile	Leu	Lys	Leu	Asn	Lys	His	Asn	Met	Thr	Val	Ile	Gln	275	280	285	
Thr	Asp	Phe	Val	Pro	Val	Thr	Pro	Tyr	Glu	Thr	Asp	Tyr	Leu	Phe	Leu	290	295	300	

Gly Ile Gly Gln Arg Ala Asp Val Leu Ile Thr Ala Asp Gln Asp Val  
 305 310 315 320  
 Asp Ser Tyr Trp Phe Asn Leu Thr Trp Pro Ser Asn Gly Leu Cys Gly  
 325 330 335  
 Ser Ser Lys Val Ser Tyr Pro Ala Ser Ile Phe Arg Tyr Glu Gly Ala  
 340 345 350  
 Thr Asp Glu Asn Pro Thr Asp Glu Gly Thr Ala Pro Ser Ser Leu Ala  
 355 360 365  
 Cys Asp Asp Lys Tyr Asp Tyr Glu Pro Val Val Thr Leu Ala Val Pro  
 370 375 380  
 Ser Glu Ser Phe Ala Glu Ser Ile Asp Ser Thr Leu Asp Val Ser Leu  
 385 390 395 400  
 Thr Thr Lys Thr Trp Glu Asn Ile Asp Ser Arg Val Tyr Trp Thr Val  
 405 410 415  
 Ser Glu Ser Ser Ile Asn Val Thr Trp Gly His Pro Thr Leu Gln Tyr  
 420 425 430  
 Ile Asn Glu Asn Asp Thr Ser Tyr Pro Thr Asp Leu Asn Val Leu Lys  
 435 440 445  
 Val Pro Asp Asn Gln Thr Trp Ala Tyr Trp Val Ile Asn Asn Glu Leu  
 450 455 460  
 Ser Val Pro His Pro Leu His Leu His Gly His Asp Phe Phe Val Leu  
 465 470 475 480  
 Gly Ser Ser Gly Thr Leu Asp Thr Ala Ala Asn Phe Asn Ala Ser Ser  
 485 490 495  
 Asp Leu Ser Ser Leu Asn Phe Lys Asn Pro Met Arg Arg Asp Val Thr  
 500 505 510  
 Met Leu Pro Gly Asn Gly Trp Val Val Met Ala Phe Glu Asn Asn Asn  
 515 520 525  
 Pro Gly Ala Trp Val Met His Cys His Ile Ala Trp His Val Ala Ser  
 530 535 540  
 Gly Leu Ser Val Gln Phe Val Glu Lys Val Asp Asp Ile Lys Ser Leu  
 545 550 555 560  
 Phe Asp Leu Ser Ser Val Leu Asp Asp Arg Cys Ser Ala Trp Asn Thr  
 565 570 575  
 Tyr Glu Ala Glu Thr Ile Tyr Lys Gln Asp Asp Ser Gly  
 580 585

&lt;210&gt; 25

&lt;211&gt; 1179

&lt;212&gt; DNA

&lt;213&gt; OUnknown

&lt;220&gt;

&lt;223&gt; Obtained from an environmental sample

&lt;400&gt; 25

gtggccacgg	tgcccgccac	cactcgggtt	ccagcagcct	tgggcaccgg	ccgggactca	60
ccagtgatca	gcgggctcgc	cgatgtcacc	aatctccaca	ctcacggctt	tcattgtttca	120
ccgcaaggga	actccgacaa	catcttcctc	cacatcaacc	ccggcgagac	cttcgactac	180
gagttcaagc	tgcccgcgaa	ccactcaccg	gggatgtact	ggtatcacc	gcatggtcac	240
ggcgacaccg	ccccccagtg	caacggcggc	atggccgggg	tgatcctgat	cgacggcggt	300
ctcgacgagg	tgccgggaat	cgccggtctg	accgaacgcc	tgctcgtcct	ccaggcgacg	360
caattcgacg	gcgacggcaa	cctcgtccct	tacaacaacc	agtcgaacgc	gactcggcag	420
cgcttcgtca	acggtcaact	caacccaacg	atcgcgattc	gaccggcgga	gacacagcgc	480
tggcgggatcg	ccaacgtcag	ctctgacaac	ttcttcctgc	tggcgctagc	tggtcacacg	540
ctgcaccaga	tcgccgcgga	cggcaaccgc	tatgacgagg	tcgttcgcgc	cgaccagatc	600
ctcctccac	cctcggagcg	ggtcggagtc	ttggtgcagg	catcgaccca	actgggaagc	660
tacgagttcc	gcaccctcct	ctggggcgac	gatttcagg	ccgaaccgga	cgtggtgctg	720
gcgacgatgg	tcgtcgtctg	cgaggcaatc	actccagcac	cgctcccaac	cgcgctcatc	780



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ccctacgagg acttgcgga tgtcccggc gacaacatcc gcgtgaccac cttcgaggaa      840
ccgggcgctc ccctctacct ggcgatcgac ggcaagcact tcgaccccga ccgcgtcgac      900
cagacgggtga agttgggggc gacggaggag tggatcgctc gcaataccag ctccgaatgg      960
caccggttcc acatccacgt caacgacttc caggtgatcg ccgtcaacaa cgaagcggtc     1020
aacacccatg gctacgagga ctccgtcgcc ctcccaccac acagcgaaac gacgatgcgg     1080
atgaaattcc tcgacttcag cggcaaattc gtctaccact gccacatcct cgggcacgaa     1140
gacttcggca tgatggcggg agtggagggt gttgagtag      1179

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&lt;210&gt; 26

&lt;211&gt; 392

&lt;212&gt; PRT

&lt;213&gt; Unknown

&lt;220&gt;

&lt;223&gt; Obtained from an environmental sample

&lt;221&gt; DOMAIN

&lt;222&gt; (108)...(249)

&lt;223&gt; Multicopper oxidase

&lt;400&gt; 26

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Met Ala Thr Val Pro Ala Thr Thr Arg Phe Pro Ala Ala Leu Gly Thr
 1          5          10          15
Gly Arg Asp Ser Pro Val Ile Ser Gly Leu Ala Asp Val Thr Asn Leu
 20          25          30
His Thr His Gly Phe His Val Ser Pro Gln Gly Asn Ser Asp Asn Ile
 35          40          45
Phe Leu His Ile Asn Pro Gly Glu Thr Phe Asp Tyr Glu Phe Lys Leu
 50          55          60
Pro Ala Asn His Ser Pro Gly Met Tyr Trp Tyr His Pro His Gly His
 65          70          75          80
Gly Asp Thr Ala Pro Gln Cys Asn Gly Gly Met Ala Gly Val Ile Leu
 85          90          95
Ile Asp Gly Gly Leu Asp Glu Val Pro Gly Ile Ala Gly Leu Thr Glu
 100         105         110
Arg Leu Leu Val Leu Gln Ala Thr Gln Phe Asp Gly Asp Gly Asn Leu
 115         120         125
Val Pro Tyr Asn Asn Gln Ser Asn Ala Thr Arg Gln Arg Phe Val Asn
 130         135         140
Gly Gln Leu Asn Pro Thr Ile Ala Ile Arg Pro Gly Glu Thr Gln Arg
 145         150         155         160
Trp Arg Ile Ala Asn Val Ser Ser Asp Asn Phe Phe Leu Leu Ala Leu
 165         170         175
Ala Gly His Thr Leu His Gln Ile Ala Ala Asp Gly Asn Pro Tyr Asp
 180         185         190
Glu Val Val Pro Arg Asp Gln Ile Leu Leu Pro Pro Ser Glu Arg Val
 195         200         205
Glu Val Leu Val Gln Ala Ser Thr Gln Leu Gly Ser Tyr Glu Phe Arg
 210         215         220
Thr Leu Leu Trp Gly Asp Asp Phe Gln Ala Glu Pro Asp Val Val Leu
 225         230         235         240
Ala Thr Met Val Val Ala Gly Glu Ala Ile Thr Pro Ala Pro Leu Pro
 245         250         255
Thr Ala Leu Ile Pro Tyr Glu Asp Leu Arg Asp Val Pro Val Asp Asn
 260         265         270
Ile Arg Val Thr Thr Phe Glu Glu Pro Gly Ala Pro Leu Tyr Leu Ala
 275         280         285
Ile Asp Gly Lys His Phe Asp Pro Asp Arg Val Asp Gln Thr Val Lys
 290         295         300

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Leu	Gly	Ala	Thr	Glu	Glu	Trp	Ile	Val	Arg	Asn	Thr	Ser	Ser	Glu	Trp
305					310					315					320
His	Pro	Phe	His	Ile	His	Val	Asn	Asp	Phe	Gln	Val	Ile	Ala	Val	Asn
			325						330						335
Asn	Glu	Ala	Val	Asn	Thr	His	Gly	Tyr	Glu	Asp	Ser	Val	Ala	Leu	Pro
			340					345					350		
Pro	His	Ser	Glu	Thr	Thr	Met	Arg	Met	Lys	Phe	Leu	Asp	Phe	Ser	Gly
		355					360					365			
Lys	Phe	Val	Tyr	His	Cys	His	Ile	Leu	Gly	His	Glu	Asp	Phe	Gly	Met
	370					375					380				
Met	Ala	Val	Val	Glu	Val	Val	Glu								
385					390										